

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Scott, Matthew P.  
Goodrich, Lisa V.  
Johnson, Ronald L.

(ii) TITLE OF INVENTION: Mammalian Patched Gene and Its Use

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
(B) STREET: 4 Embarcadero Center, Suite 3400  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-4187

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Rowland, Bertram I  
(B) REGISTRATION NUMBER: 20,015  
(C) REFERENCE/DOCKET NUMBER: A60190/BIR STAN171

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 680 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACCTATGGC ACCCCCCCCC ACCTTCCCTA ACAAAACCCC TTTATACCCC CTTAAATT

CCACCCAAAC CCTAACAGA AACTTTTA ACCCCCCCA CCCGGAATTC CATCCCCCCC

60

120

AAATTACAAC	TCCAGCCAAA	ATTAAAATTG	GTCCTAACCT	AACCATGTTG	TTACGGTTTC	180
CCCCCCCCAAA	TACATGCACT	GGCCCGAACCA	CTTGATCGTT	GCCGTTCCAA	TAAGAATAAA	240
TCTGGTCATA	TTAAACAAAGC	CAAAGCTTTA	CAAACGTGTTG	TACAATTAAT	GGCGAACAC	300
GAACGTTCG	AATTCTGGTC	TGGACATTAC	AAAGTGCACC	ACATCGGATG	GAACCAGGAG	360
AAGGCCACAA	CCGTACTGAA	CGCCTGGCAG	AAGAAGTTCG	CACAGGTTGG	TGGTTGGCGC	420
AAGGAGTAGA	GTGAATGGTG	GTAATTTTG	GTTGTTCCAG	GAGGTGGATC	GTCTGACGAA	480
GAGCAAGAAG	TCGTCGAATT	ACATCTTCGT	GACGTTCTCC	ACCGCCAATT	TGAACAAGAT	540
GTTGAAGGAG	GCGTCGAAAC	GGACGTGGTG	AAGCTGGGGG	TGGTGCTGGG	GGTGGCGGCG	600
GTGTACGGGT	GGGTGGCCCA	GTCGGGGCTG	GCTGCCTTGG	GAGTGCTGGT	CTTGCGGCTC	660
ATTGCCCTA	TAGTAGCGTA					680

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Pro	Pro	Pro	Asn	Tyr	Asn	Ser	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Leu	Val
1					5					10					15
Leu	Thr	Pro	Xaa	Val	Val	Thr	Val	Ser	Pro	Pro	Lys	Tyr	Met	His	Trp
			20				25						30		
Pro	Glu	His	Leu	Ile	Val	Ala	Val	Pro	Ile	Arg	Ile	Asn	Leu	Val	Ile
			35				40						45		
Leu	Asn	Lys	Pro	Lys	Ala	Leu	Gln	Thr	Val	Val	Gln	Leu	Met	Gly	Glu
			50			55					60				
His	Glu	Leu	Phe	Glu	Phe	Trp	Ser	Gly	His	Tyr	Lys	Val	His	His	Ile
			65			70			75						80
Gly	Trp	Asn	Gln	Glu	Lys	Ala	Thr	Thr	Val	Leu	Asn	Ala	Trp	Gln	Lys
			85					90						95	
Lys	Phe	Ala	Gln	Val	Gly	Gly	Trp	Arg	Lys	Glu					
			100					105							

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAGTGTC GACACGCTGT TAAAGGTGTTA CGAAACTATC GAAACTCTGT ACCGTTCCGT	60
GTTACATTGCG TGCAGTGATA AACAGAAGTG AATAATTCCGG GTGTACAAGT GTGTGGTTAT	120
GTGGCGGCCGA GTGATATGAC AGCGTGCGCC GCCAGACGGA TTCCAGCCGT CTTCATGAGG	180
ATATCGGTGA CAAGCCTGGC CCCGAGATCA TGGTGGCTCC CGATTCCGAG GCTCCTTCGA	240
ATCCTCGGAT AACGGCTGCA CACGAGAGCC CCTGCGCCAC CGAGGCGCGC CACAGTGCTG	300
ATCTTTACAT ACGTACCAGT TGGGTGGACG CCGCACTAGC TCTCTCTGAA CTCGAAAAGG	360
GTAACATCGA AGGAGGAAGA ACCTCTCTGT GGATACGAGC GTGGCTACAA GAACAGCTCT	420
TTATTTGGG CTGCTTTCTT CAAGGCGACG CGGGGAAAGT CCTCTTCGTT GCCATCCTCG	480
TTCTGTCGAC GTTCTGCGTC GGTCTCAAGT CAGCACAAAT ACATACAAGG GTCGACCAAC	540
TCTGGGTTCA AGAGGGTGGT AGATTAGAAG CCGAGTTGAA ATATACAGCG CAAGCTTTGG	600
GCGAGGCGGA CTCCTCGACG CACCAGCTTG TCATACAAAC TGCCAAAGAT CCAGACGTCT	660
CCCTGCTACA TCCAGGCGCG TTGCTTGAAC ACCTTAAGGT GGTGCACGCA GCGACTCGGG	720
TGACAGTTCA CATGTACGAC ATTGAGTGGC GCCTCAAAGA CCTGTGCTAC AGCCCCAGCA	780
TACCGGACTT CGAGGGTTAC CACCACATCG AGTCAATCAT AGACAACGTC ATCCCCTGCG	840
CTATTATCAC CCCCCTTGAT TGCTTCTGGG AAGGCTCCAA GTTGCTTGGT CCCGATTATC	900
CTATATACGT ACCACATCTT AAACACAAAC TACAATGGAC ACATTTAAAT CCATTGGAAG	960
TTGTAGAAGA AGTAAAAAAA TTAAAGTTCC AATTTCTCT GAGCACAATA GAGGCGTACA	1020
TGAAGAGAGC CGGCATCACT TCCGCCTACA TGAAAAAGCC GTGCTTAGAC CCCACCGACC	1080
CACATTGTCC AGCCACGGCT CCAAACAAAA AGTCTGGTCA TATTCCAGAT GTAGCGGCGG	1140
AGCTGTCGCA CGGATGTTAT GGTTCGCGG CAGCTTACAT GCACTGGCCG GAACAGTTAA	1200
TTGTAGGGGG AGCTACAAGG AATTCGACAT CAGCTCTGAG AAAAGCACGC GTTTACAGAC	1260
TGTAGTACAG TTAATGGCG AGAGAGAAAT GTACGAGTAC TGGGCCGATC ATTATAAAGT	1320
ACATCAAATT GGCTGGAATC AAGAGAAGGC AGCTGCTGTA CTGGATGCCT GGCAGAGAAA	1380
GTGGCCGCT GAAGTCAGAA AAATTACTAC CTCAGGATCA GTATCATCGG CTTATAGTT	1440

CTATCCGTTTC	TCCACCTCGA	CACTTAATGA	CATACTCGGG	AAGTTCTCCG	AAGTGTCACT	1500
GAAGAACATT	ATATTAGGCT	ATATGTTAT	GTTAATTAT	GTTGCCGTTA	CTTTAATACA	1560
ATGGCGGGAT	CCGATTCGCT	CGCAAGCGGG	TGTGGGTATC	GCCGGAGTTC	TACTACTATC	1620
AATCACTGTT	GCCGCTGGCT	TAGGATTTG	TGCTTTATTA	GGCATACCAT	TCAACGCTTC	1680
AAGTACGCAA	ATAGTACCAT	TCCTAGCGCT	CGGGTTAGGA	GTTCAAGATA	TGTTTCTTCT	1740
CACTCACACG	TATGTGGAGC	AAGCGGGAGA	TGTGCCTAGA	GAAGAGAGGA	CTGGACTTGT	1800
ATTGAAAAAG	AGCGGTTAA	GCGTACTTCT	GGCGTCTTG	TGCAACGTGA	TGGCATTTTT	1860
GGCAGCAGCC	CTTCTACCTA	TTCCAGCTTT	CAGAGTATT	TGCCTACAGG	CTGCCATACT	1920
TCTTCTGTTT	AACTTGGGT	CAATATTACT	GGTTTTCTCT	GCTATGATCT	CGTTAGACCT	1980
GCGACGGAGG	TCAGCCGCGA	GGGCCGATCT	TTTATGCTGT	TTGATGCCTG	AGAGTCCATT	2040
ACCGAAGAAG	AAAATTCCGG	AAAGAGAAA	AACTAGAAAA	AACGATAAGA	CTCATAGGAT	2100
AGACACCACG	AGACAACCTC	TAGACCCAGA	TGTGTCCGAG	AACGTGACCA	AAACTTGCTG	2160
CTTAAGCGTC	TCGCTCACCA	AGTGGGCCAA	GAACCAATAC	GCGCCGTTCA	TCATGCGCCC	2220
CGCTGTTAAG	GTTACATCCA	TGTTAGCGTT	GATTGCTGTT	ATTCTGACTA	GCGTTGGGG	2280
AGCGACAAAAA	GTAAAGGATG	GATTGGATT	GACTGATATT	GTACCGGAGA	ATACAGACGA	2340
ACACGAATT	TTATCTCGTC	AGGAAAATA	CTTTGGCTTC	TATAATATGT	ACGCCGTGAC	2400
GCAAGGCAAC	TTTGAATATC	CCACCAATCA	GAAGTTATTA	TATGAGTATC	ACGATCAATT	2460
CGTCAGAATA	CCTAATATAA	TCAAGAATGA	TAACGGCGGT	CTCACGAAAT	TTGGTTGAG	2520
TTTATTCCGC	GAETGGTTAT	TGGACTTGCA	AGTGGCTTT	GATAAGGAGG	TTGCCAGCGG	2580
TTGTATAACA	CAAGAGTATT	GGTGCAAAAAA	CGCGAGTGAC	GAAGGAATAT	TGGCCTATAA	2640
ACTTATGGTG	CAGACTGGCC	ATGTGGACAA	TCCAATCGAT	AAGTCTCTGA	TTACGGCAGG	2700
TCACAGACTA	GTTGACAAAG	ACGGTATTAT	AAATCCAAAG	GCATTTATA	ATTACCTATC	2760
AGCTTGGGCT	ACTAACGACG	CGTTGGCATA	CGGAGCCTCA	CAAGGGAAC	TGAAACCTCA	2820
GCCCCAAAGA	TGGATCCATT	CTCCGGAGGA	TGTACATT	GAAATAAAGA	AATCGTCGCC	2880
ATTAATTAC	ACACAGTTAC	CATTCTACCT	TTCCGGTCTC	AGCGACACTA	TAGCATCAA	2940
ACGTTGATAA	GATCTGTGCG	AGATTATGT	CTGAAGTACG	AGGCAGAAAGG	TTTACCGAAC	3000
TTTCCATCGG	GTATACCATT	CCTTTCTGG	GAACAGTATT	TGTATTAAAG	GACATCTTA	3060
CTACTGGCTT	TGGCGTGTGC	TTTGGCAGCT	GTCTTCATTG	CGGTTATGGT	GCTATTGTTG	3120
AACGCCTGGG	CAGCAGTACT	GGTGACATTA	GCGCTGGCTA	CATTAGTACT	GCAGCTGTTA	3180

GGTGTATGGC CTTATTGGGC GTGAAGCTAT CTGCAATGCC GGCGTACTA CTGGTGCTAG	3240
CCATTGGAG AGGAGTTCAC TTCACTGTGC ATTTATGTTT GGGTTTGTA ACATCAATCG	3300
GTTGCAAGCG GCGCCGCGCG TCACTAGCTC TAGAACAGT TCTGGCGCCA GTGGTGCACG	3360
GCGCTCTGGC GGCGCGCTG GCTGCCTCGA TGCTAGCTGC AAGTGAATGT GGCTTCGTTG	3420
CCAGACTGTT CTTGAGGTTA CTACTGGACA TCGTGTTCT GGGACTCATC GATGGGTTGC	3480
TGTTCTTCCC TATTGTCCTT TCGATATTGG GACCGGCTGC TGAGGTACGA CCTATAGAGC	3540
ATCCAGAACG CTTATCGACT CCATCGCAA AATGTTGCC CATCCACCCT CGCAAATCAA	3600
GTTCCAGCTC AGGCGGTGGT GATAAATCAA GTCGAACCAAG TAAATCAGCA CCAAGGCCTT	3660
GCGCACCATC TCTCACGACC ATTACTGAAG AGCCTCGAG TTGGCACAGT TCCGCCACT	3720
CCGTACAATC TTCTATGCAG TCGATAGTGG TCCAGCCGA GGTGGTGGTC GAAACTACCA	3780
CGTATAATGG CAGCGATTCT GCTTCAGGAC GGTGACGCC TACAAAGTCT TCACACGGTG	3840
GTGCTATCAC AACTACTAAG GTGACCGCCA CGGCAAATAT AAAGGTAGAA GTGGTGACAC	3900
CGAGTGACAG GAAATCGCGA CGTTCTATC ATTACTATGA TCGTCGAAGG GATCGCGATG	3960
AAGATAGGGA TCGAGACCGT GAAAGGGACA GAGATCGCGA CAGGGATCGG GATAGGGATC	4020
GTGACCGGGA CAGGGATAAG GATAGAGAAC GATCGAGAGA ACGAGACAGG CGAGACCGAT	4080
ATAGAGACGA AAGGGACAC CGAGCTTCGC CGAGAGAAAA ACGGCAGAGA TTCTGGACAT	4140
GAAAGTGATT CATCACGTCA TTAAGGATGA AGTACATTGC CAACTGCCA GAAACGCTCG	4200
TACAGTCGCG GTATCTGAAC ATATACCGGT TCGTTATTG AATAACTTGT AAATGATCTC	4260
TTTGATTCGG CTTAACATA TTTTAGTTCA CATCCTGCAA CATCTTAATA CGGTTAGGGT	4320
TAATTTAAG TCCATAATAG TCGTATGTGG TTGGTCCTTG CGTTAAGTGC ATTAGTTTT	4380
TCCCCATCACT GGGTCCGTGG CTTTAATTG GGTTAACGG GGGGGGACCT TTTTTTTTT	4440
TTTTTTTG	4448

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1311 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ala Pro Asp Ser Glu Ala Pro Ser Asn Pro Arg Ile Thr Ala  
 1 5 10 15  
 Ala His Glu Ser Pro Cys Ala Thr Glu Ala Arg His Ser Ala Asp Leu  
 20 25 30  
 Tyr Ile Arg Thr Ser Trp Val Asp Ala Ala Leu Ala Leu Ser Glu Leu  
 35 40 45  
 Glu Lys Gly Asn Ile Glu Gly Gly Arg Thr Ser Leu Trp Ile Arg Ala  
 50 55 60  
 Trp Leu Gln Glu Gln Leu Phe Ile Leu Gly Cys Phe Leu Gln Gly Asp  
 65 70 75 80  
 Ala Gly Lys Val Leu Phe Val Ala Ile Leu Val Leu Ser Thr Phe Cys  
 85 90 95  
 Val Gly Leu Lys Ser Ala Gln Ile His Thr Arg Val Asp Gln Leu Trp  
 100 105 110  
 Val Gln Glu Gly Arg Leu Glu Ala Glu Leu Lys Tyr Thr Ala Gln  
 115 120 125  
 Ala Leu Gly Glu Ala Asp Ser Ser Thr His Gln Leu Val Ile Gln Thr  
 130 135 140  
 Ala Lys Asp Pro Asp Val Ser Leu Leu His Pro Gly Ala Leu Leu Glu  
 145 150 155 160  
 His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr  
 165 170 175  
 Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro  
 180 185 190  
 Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile  
 195 200 205  
 Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys  
 210 215 220  
 Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys  
 225 230 235 240  
 Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys  
 245 250 255  
 Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Ile Glu Ala Tyr Met Lys  
 260 265 270  
 Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro  
 275 280 285  
 Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His  
 290 295 300  
 Ile Pro Asp Val Ala Ala Glu Leu Ser His Gly Cys Tyr Gly Phe Ala

305	310	315	320
Ala Ala Tyr Met His Trp Pro Glu Gln Leu Ile Val Gly Gly Ala Thr			
325                           330                           335			
Arg Asn Ser Thr Ser Ala Leu Arg Lys Ala Arg Xaa Leu Gln Thr Val			
340                           345                           350			
Val Gln Leu Met Gly Glu Arg Glu Met Tyr Glu Tyr Trp Ala Asp His			
355                           360                           365			
Tyr Lys Val His Gln Ile Gly Trp Asn Gln Glu Lys Ala Ala Ala Val			
370                           375                           380			
Leu Asp Ala Trp Gln Arg Lys Phe Ala Ala Glu Val Arg Lys Ile Thr			
385                           390                           395                           400			
Thr Ser Gly Ser Val Ser Ser Ala Tyr Ser Phe Tyr Pro Phe Ser Thr			
405                           410                           415			
Ser Thr Leu Asn Asp Ile Leu Gly Lys Phe Ser Glu Val Ser Leu Lys			
420                           425                           430			
Asn Ile Ile Leu Gly Tyr Met Phe Met Leu Ile Tyr Val Ala Val Thr			
435                           440                           445			
Leu Ile Gln Trp Arg Asp Pro Ile Arg Ser Gln Ala Gly Val Gly Ile			
450                           455                           460			
Ala Gly Val Leu Leu Leu Ser Ile Thr Val Ala Ala Gly Leu Gly Phe			
465                           470                           475                           480			
Cys Ala Leu Leu Gly Ile Pro Phe Asn Ala Ser Ser Thr Gln Ile Val			
485                           490                           495			
Pro Phe Leu Ala Leu Gly Leu Gly Val Gln Asp Met Phe Leu Leu Thr			
500                           505                           510			
His Thr Tyr Val Glu Gln Ala Gly Asp Val Pro Arg Glu Glu Arg Thr			
515                           520                           525			
Gly Leu Val Leu Lys Lys Ser Gly Leu Ser Val Leu Leu Ala Ser Leu			
530                           535                           540			
Cys Asn Val Met Ala Phe Leu Ala Ala Ala Leu Leu Pro Ile Pro Ala			
545                           550                           555                           560			
Phe Arg Val Phe Cys Leu Gln Ala Ala Ile Leu Leu Leu Phe Asn Leu			
565                           570                           575			
Gly Ser Ile Leu Leu Val Phe Pro Ala Met Ile Ser Leu Asp Leu Arg			
580                           585                           590			
Arg Arg Ser Ala Ala Arg Ala Asp Leu Leu Cys Cys Leu Met Pro Glu			
595                           600                           605			
Ser Pro Leu Pro Lys Lys Lys Ile Pro Glu Arg Ala Lys Thr Arg Lys			
610                           615                           620			

Asn Asp Lys Thr His Arg Ile Asp Thr Thr Arg Gln Pro Leu Asp Pro  
625 630 635 640

Asp Val Ser Glu Asn Val Thr Lys Thr Cys Cys Leu Ser Val Ser Leu  
645 650 655

Thr Lys Trp Ala Lys Asn Gln Tyr Ala Pro Phe Ile Met Arg Pro Ala  
660 665 670

Val Lys Val Thr Ser Met Leu Ala Leu Ile Ala Val Ile Leu Thr Ser  
675 680 685

Val Trp Gly Ala Thr Lys Val Lys Asp Gly Leu Asp Leu Thr Asp Ile  
690 695 700

Val Pro Glu Asn Thr Asp Glu His Glu Phe Leu Ser Arg Gln Glu Lys  
705 710 715 720

Tyr Phe Gly Phe Tyr Asn Met Tyr Ala Val Thr Gln Gly Asn Phe Glu  
725 730 735

Tyr Pro Thr Asn Gln Lys Leu Leu Tyr Glu Tyr His Asp Gln Phe Val  
740 745 750

Arg Ile Pro Asn Ile Ile Lys Asn Asp Asn Gly Gly Leu Thr Lys Phe  
755 760 765

Trp Leu Ser Leu Phe Arg Asp Trp Leu Leu Asp Leu Gln Val Ala Phe  
770 775 780

Asp Lys Glu Val Ala Ser Gly Cys Ile Thr Gln Glu Tyr Trp Cys Lys  
785 790 795 800

Asn Ala Ser Asp Glu Gly Ile Leu Ala Tyr Lys Leu Met Val Gln Thr  
805 810 815

Gly His Val Asp Asn Pro Ile Asp Lys Ser Leu Ile Thr Ala Gly His  
820 825 830

Arg Leu Val Asp Lys Asp Gly Ile Ile Asn Pro Lys Ala Phe Tyr Asn  
835 840 845

Tyr Leu Ser Ala Trp Ala Thr Asn Asp Ala Leu Ala Tyr Gly Ala Ser  
850 855 860

Gln Gly Asn Leu Lys Pro Gln Pro Gln Arg Trp Ile His Ser Pro Glu  
865 870 875 880

Asp Val His Leu Glu Ile Lys Lys Ser Ser Pro Leu Ile Tyr Thr Gln  
885 890 895

Leu Pro Phe Tyr Leu Ser Gly Leu Ser Asp Thr Xaa Ser Ile Lys Thr  
900 905 910

Leu Ile Arg Ser Val Arg Asp Leu Cys Leu Lys Tyr Glu Ala Lys Gly  
915 920 925

Leu Pro Asn Phe Pro Ser Gly Ile Pro Phe Leu Phe Trp Glu Gln Tyr

930	935	940	
Leu Tyr Leu Arg Thr Ser	Leu Leu Leu Ala	Leu Ala Cys Ala Leu Ala	
945	950	955	960
Ala Val Phe Ile Ala Val Met	Val Leu Leu Asn Ala Trp	Ala Ala	
965	970	975	
Val Leu Val Thr Leu Ala	Leu Ala Thr Leu Val Leu Gln	Leu Leu Gly	
980	985	990	
Val Met Ala Leu Leu Gly	Val Lys Leu Ser Ala Met	Pro Ala Val Leu	
995	1000	1005	
Leu Val Leu Ala Ile Gly	Arg Gly Val His Phe Thr	Val His Leu Cys	
1010	1015	1020	
Leu Gly Phe Val Thr Ser	Ile Gly Cys Lys Arg Arg	Arg Ala Ser Leu	
1025	1030	1035	1040
Ala Leu Glu Ser Val Leu Ala Pro	Val Val His Gly Ala	Leu Ala Ala	
1045	1050	1055	
Ala Leu Ala Ala Ser Met	Leu Ala Ser Glu Cys Gly	Phe Val Ala	
1060	1065	1070	
Arg Leu Phe Leu Arg	Leu Leu Asp Ile Val Phe	Leu Gly Leu Ile	
1075	1080	1085	
Asp Gly Leu Leu Phe Phe	Pro Ile Val Leu Ser	Ile Leu Gly Pro Ala	
1090	1095	1100	
Ala Glu Val Arg Pro Ile	Glu His Pro Glu Arg	Leu Ser Thr Pro Ser	
1105	1110	1115	1120
Pro Lys Cys Ser Pro Ile	His Pro Arg Lys Ser	Ser Ser Ser Ser Gly	
1125	1130	1135	
Gly Gly Asp Lys Ser Ser	Arg Thr Ser Lys Ser	Ala Pro Arg Pro Cys	
1140	1145	1150	
Ala Pro Ser Leu Thr Thr	Ile Thr Glu Glu Pro Ser	Ser Trp His Ser	
1155	1160	1165	
Ser Ala His Ser Val Gln	Ser Ser Met Gln Ser	Ile Val Val Gln Pro	
1170	1175	1180	
Glu Val Val Val Glu Thr	Thr Thr Tyr Asn Gly	Ser Asp Ser Ala Ser	
1185	1190	1195	1200
Gly Arg Ser Thr Pro Thr	Lys Ser Ser His Gly	Gly Ala Ile Thr Thr	
1205	1210	1215	
Thr Lys Val Thr Ala Thr	Ala Asn Ile Lys Val	Glu Val Val Thr Pro	
1220	1225	1230	
Ser Asp Arg Lys Ser Arg	Arg Ser Tyr His Tyr	Tyr Asp Arg Arg Arg	
1235	1240	1245	

Asp Arg Asp Glu Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg  
1250 1255 1260

Asp Arg  
1265 1270 1275 1280

Glu Arg Ser Arg Glu Arg Asp Arg Arg Asp Arg Tyr Arg Asp Glu Arg  
1285 1290 1295

Asp His Arg Ala Ser Pro Arg Glu Lys Arg Gln Arg Phe Trp Thr  
1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAACAAGA GAGCGAGTGA GAGTAGGGAG AGCGTCTGTG TTGTGTGTTG AGTGTGCC	60
ACGCACACAG GCGCAAAACA GTGCACACAG ACGCCGCTG GGCAAGAGAG AGTGAGAGAG	120
AGAACACAGCG GCGCGCGCTC GCCTAATGAA GTTGTGAGCC TGGCTGGCGT GCCGCATCCA	180
CGAGATACAG ATACATCTCT CATGGACCAG GACAGCCTCC CACGCGTTCC GGACACACAC	240
GGCGATGTGG TCGATGAGAA ATTATTCTCG GATCTTACA TACGCACCAAG CTGGGTGGAC	300
GCCCAAGTGG CGCTCGATCA GATACTAAAG GGCAGAGCGC GTGGCAGCCG CACGGCGATC	360
TATCTGCGAT CAGTATTCCA GTCCCACCTC GAAACCCTCG GCAGCTCCGT GCAAAAGCAC	420
CGGGGCAAGG TGCTATTCTG GGCTATCCTG GTGCTGAGCA CCTTCTGCGT CGGCCTGAAG	480
AGCGCCCAGA TCCACTCCAA GGTGCACCAAG CTGTGGATCC AGGAGGGCGG CCGGCTGGAG	540
GCGGAACCTGG CCTACACACA GAAGACGATC GGGGAGGACG AGTCGGCCAC GCATCAGCTG	600
CTCATTCTAGA CGACCCACGA CCCGAACGCC TCCGTCTGC ATCCGCAGGC GCTGCTTGGC	660
CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC ACCTCTACGA CACCGAATGG	720
GGGCTGGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT TCGAGGGCAT CTACTACATC	780
GAGCAGATCC TGCGCCACCT CATTCCGTGC TCGATCATCA CGCCGCTGGA CTGTTCTGG	840
GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA TACCAGGCCT CAACCAACGA	900
CTCCTGTGGA CCACCCCTGAA TCCCGCCTCT GTGATGCAGT ATATGAAACA AAAGATGTCC	960

GAGGAAAAGA	TCAGCTTCGA	CTTCGAGACC	GTGGAGCAGT	ACATGAAGCG	TGCGGCCATT	1020
GGCAGTGGCT	ACATGGAGAA	GCCCTGCCTG	AACCCACTGA	ATCCCAATTG	CCCGGACACG	1080
GCACCGAACCA	AGAACAGCAC	CCAGCCGCCG	GATGTGGGAG	CCATCCTGTC	CGGAGGCTGC	1140
TACGGTTATG	CCCGAAGCA	CATGCACTGG	CCGGAGGAGC	TGATTGTGGG	CGGACGGAAG	1200
AGGAACCGCA	GCGGACACTT	GAGGAAGGCC	CAGGCCCTGC	AGTCGGTGGT	GCAGCTGATG	1260
ACCGAGAAGG	AAATGTACGA	CCAGTGGCAG	GACAAC TACA	AGGTGCACCA	TCTTGGATGG	1320
ACGCAGGAGA	AGGCAGCGGA	GGTTTGAAAC	GCCTGGCAGC	GCAACTTTTC	GC GGGAGGTG	1380
GAACAGCTGC	TACGTAAACA	GTCGAGAATT	GCCACCAACT	ACGATATCTA	CGTGTTCAGC	1440
TCGGCTGCAC	TGGATGACAT	CCTGGCCAAG	TTCTCCCATC	CCAGCGCCTT	GTCCATTGTC	1500
ATCGGCGTGG	CCGTCACCGT	TTTGTATGCC	TTTGCACGC	TCCTCCGCTG	GAGGGACCCC	1560
GTCCGTGGCC	AGAGCAGTGT	GGGCGTGGCC	GGAGTTCTGC	TCATGTGCTT	CAGTACCGCC	1620
GCCGGATTGG	GATTGTCAGC	CCTGCTCGGT	ATCGTTTCA	ATGCGCTGAC	CGCTGCCTAT	1680
GCGGAGAGCA	ATCGGCGGGA	GCAGACCAAG	CTGATTCTCA	AGAACGCCAG	CACCCAGGTG	1740
GTTCCGTTTT	TGGCCCTTGG	TCTGGCGTC	GATCACATCT	TCATAGTGGG	ACCGAGCATC	1800
CTGTTCA GTG	CCTGCAGCAC	CGCAGGATCC	TTCTTGCGG	CCGCCTTAT	TCCGGTGCCG	1860
GCTTTGAAGG	TATTCTGTCT	GCAGGCTGCC	ATCGTAATGT	GCTCCAATT	GGCAGCGGCT	1920
CTATTGGTTT	TTCCGGCCAT	GATTCGTTG	GATCTACGGA	GACGTACCGC	CGGCAGGGCG	1980
GACATTTCT	GCTGCTGTTT	TCCGGTGTGG	AAGGAACAGC	CGAAGGTGGC	ACCTCCGGTG	2040
CTGCCGCTGA	ACAACAACAA	CGGGCGCGGG	GCCC GGCA TC	CGAAGAGCTG	CAACAACAAC	2100
AGGGTGCCGC	TGCCCGCCCA	GAATCCTCTG	CTGGAACAGA	GGGCAGACAT	CCCTGGGAGC	2160
AGTCACTCAC	TGGCGTCCTT	CTCCCTGGCA	ACCTTCGCCT	TTCAGCACTA	CACTCCCTTC	2220
CTCATGCGCA	GCTGGGTGAA	GTTCTGACC	GTATGGGTT	TCCTGGCGGC	CCTCATATCC	2280
AGCTTGTATG	CCTCCACGCG	CCTTCAGGAT	GGCCTGGACA	TTATTGATCT	GGTGCCAAG	2340
GACAGCAACG	AGCACAAGTT	CCTGGATGCT	CAAAC TCGGC	TCTTGCGCTT	CTACAGCATG	2400
TATGCGGTTA	CCCAGGGCAA	CTTTGAATAT	CCCACCCAGC	AGCAGTTGCT	CAGGGACTAC	2460
CATGATT CCT	TTGTGCGGGT	GCCACATGTG	ATCAAGAATG	ATAACGGTGG	ACTGCCGGAC	2520
TTCTGGCTGC	TGCTCTTCAG	CGAGTGGCTG	GGTAATCTGC	AAAAGATATT	CGACGAGGAA	2580
TACCGCGACG	GACGGCTGAC	CAAGGAGTGC	TGGTTCCCAA	ACGCCAGCAG	CGATGCCATC	2640
CTGGCCTACA	AGCTAATCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGGA	CAAGGAACTG	2700

GTGCTCACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCGC	CTTCTACAAC	2760
TATCTGTCGG	CATGGGCCAC	CAACGACGTC	TTCGCCTACG	GAGCTTCTCA	GGCAAATTG	2820
TATCCGGAAC	CGCGCCAGTA	TTTCACCAA	CCCAACGAGT	ACGATCTAA	GATAACCAAG	2880
AGTCTGCCAT	TGGTCTACGC	TCAGATGCC	TTTACCTCC	ACGGACTAAC	AGATACCTCG	2940
CAGATCAAGA	CCCTGATAGG	TCATATTCGC	GACCTGAGCG	TCAAGTACGA	GGGCTTCGGC	3000
CTGCCAACT	ATCCATCGGG	CATTCCCTTC	ATCTTCTGGG	AGCAGTACAT	GACCCTGCGC	3060
TCCTCACTGG	CCATGATCCT	GGCCTGCGTG	CTACTCGCCG	CCCTGGTGCT	GGTCTCCCTG	3120
CTCCTGCTCT	CCGTTGGGC	CGCCGTTCTC	GTGATCCTCA	GCGTTCTGGC	CTCGCTGGCC	3180
CAGATCTTG	GGGCATGAC	TCTGCTGGC	ATCAAACCT	CGGCCATTCC	GGCAGTCATA	3240
CTCATCCTCA	GCGTGGGCAT	GATGCTGTGC	TTCAATGTGC	TGATATCACT	GGGCTTCATG	3300
ACATCCGTTG	GCAACCGACA	GCGCCGCGTC	CAGCTGAGCA	TGCAGATGTC	CCTGGGACCA	3360
CTTGTCCACG	GCATGCTGAC	CTCCGGAGTG	GCCGTGTTCA	TGCTCTCCAC	GTCGCCCTT	3420
GAGTTTGTGA	TCCGGCACTT	CTGCTGGCTT	CTGCTGGTGG	TCTTATGCGT	TGGCGCCTGC	3480
AACAGCCTTT	TGGTGTCCC	CATCCTACTG	AGCATGGTGG	GACCGGAGGC	GGAGCTGGTG	3540
CCGCTGGAGC	ATCCAGACCG	CATATCCACG	CCCTCTCCGC	TGCCC GTGCG	CAGCAGCAAG	3600
AGATCGGGCA	AATCCTATGT	GGTGCAGGGA	TCGCGATCCT	CGCGAGGCAG	CTGCCAGAAAG	3660
TCGCATCACC	ACCACCACAA	AGACCTTAAT	GATCCATCGC	TGACGACGAT	CACCGAGGAG	3720
CCGCAGTCGT	GGAAGTCCAG	CAACTCGTCC	ATCCAGATGC	CCAATGATTG	GACCTACCAG	3780
CCGGGGAAAC	AGCGACCCGC	CTCCTACGCG	GCCCCGCC	CCGCCTATCA	CAAGGCCGCC	3840
GCCCAGCAGC	ACCACCAGCA	TCAGGGCCCG	CCCACAACGC	CCCCGCCTCC	CTTCCCGACG	3900
GCCTATCCGC	CGGAGCTGCA	GAGCATCGT	GTGCAGCCGG	AGGTGACGGT	GGAGACGACG	3960
CACTCGGACA	GCAACACCCAC	CAAGGTGACG	GCCACGGCCA	ACATCAAGGT	GGAGCTGGCC	4020
ATGCCCGGCA	GGCGGTGCG	CAGCTATAAC	TTTACGAGTT	AGCACTAGCA	CTAGTTCCCTG	4080
TAGCTATTAG	GACGTATCTT	TAGACTCTAG	CCTAAGCCGT	AACCCTATT	GTATCTGTAA	4140
AATCGATTG	TCCAGCGGGT	CTGCTGAGGA	TTTCGTTCTC	ATGGATTCTC	ATGGATTCTC	4200
ATGGATGCTT	AAATGGCATG	GTAATTGGCA	AAATATCAAT	TTTGTTGTCT	AAAAAAGATG	4260
CATTAGCTTA	TGGTTCAAG	ATACATT	AAAGAGTCCG	CCAGATATT	ATATAAAAAA	4320
AATCCAAAAT	CGACGTATCC	ATGAAAATTG	AAAAGCTAAG	CAGACCCGTA	TGTATGTATA	4380
TGTGTATGCA	TGTTAGTTAA	TTTCCCGAAG	TCCGGTATT	ATAGCAGCTG	CCTT	4434

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Arg	Asp	Ser	Leu	Pro	Arg	Val	Pro	Asp	Thr	His	Gly	Asp	Val
1				5					10				15		
Val	Asp	Glu	Lys	Leu	Phe	Ser	Asp	Leu	Tyr	Ile	Arg	Thr	Ser	Trp	Val
		20						25					30		
Asp	Ala	Gln	Val	Ala	Leu	Asp	Gln	Ile	Asp	Lys	Gly	Lys	Ala	Arg	Gly
		35					40				45				
Ser	Arg	Thr	Ala	Ile	Tyr	Leu	Arg	Ser	Val	Phe	Gln	Ser	His	Leu	Glu
	50				55				60						
Thr	Leu	Gly	Ser	Ser	Val	Gln	Lys	His	Ala	Gly	Lys	Val	Leu	Phe	Val
65					70				75				80		
Ala	Ile	Leu	Val	Leu	Ser	Thr	Phe	Cys	Val	Gly	Leu	Lys	Ser	Ala	Gln
			85					90				95			
Ile	His	Ser	Lys	Val	His	Gln	Leu	Trp	Ile	Gln	Glu	Gly	Arg	Leu	
	100						105				110				
Glu	Ala	Glu	Leu	Ala	Tyr	Thr	Gln	Lys	Thr	Ile	Gly	Glu	Asp	Glu	Ser
	115						120				125				
Ala	Thr	His	Gln	Leu	Leu	Ile	Gln	Thr	Thr	His	Asp	Pro	Asn	Ala	Ser
	130					135				140					
Val	Leu	His	Pro	Gln	Ala	Leu	Leu	Ala	His	Leu	Glu	Val	Leu	Val	Lys
145					150				155				160		
Ala	Thr	Ala	Val	Lys	Val	His	Leu	Tyr	Asp	Thr	Glu	Trp	Gly	Leu	Arg
	165							170				175			
Asp	Met	Cys	Asn	Met	Pro	Ser	Thr	Pro	Ser	Phe	Glu	Gly	Ile	Tyr	Tyr
	180							185				190			
Ile	Glu	Gln	Ile	Leu	Arg	His	Leu	Ile	Pro	Cys	Ser	Ile	Ile	Thr	Pro
	195						200				205				
Leu	Asp	Cys	Phe	Trp	Glu	Gly	Ser	Gln	Leu	Leu	Gly	Pro	Glu	Ser	Ala
	210					215				220					
Val	Val	Ile	Pro	Gly	Leu	Asn	Gln	Arg	Leu	Leu	Trp	Thr	Thr	Leu	Asn
225					230				235				240		

Pro Ala Ser Val Met Gln Tyr Met Lys Gln Lys Met Ser Glu Glu Lys  
 245 250 255

Ile Ser Phe Asp Phe Glu Thr Val Glu Gln Tyr Met Lys Arg Ala Ala  
 260 265 270

Ile Gly Ser Gly Tyr Met Glu Lys Pro Cys Leu Asn Pro Leu Asn Pro  
 275 280 285

Asn Cys Pro Asp Thr Ala Pro Asn Lys Asn Ser Thr Gln Pro Pro Asp  
 290 295 300

Val Gly Ala Ile Leu Ser Gly Gly Cys Tyr Gly Tyr Ala Ala Lys His  
 305 310 315 320

Met His Trp Pro Glu Glu Leu Ile Val Gly Gly Arg Lys Arg Asn Arg  
 325 330 335

Ser Gly His Leu Arg Lys Ala Gln Ala Leu Gln Ser Val Val Gln Leu  
 340 345 350

Met Thr Glu Lys Glu Met Tyr Asp Gln Trp Gln Asp Asn Tyr Lys Val  
 355 360 365

His His Leu Gly Trp Thr Gln Glu Lys Ala Ala Glu Val Leu Asn Ala  
 370 375 380

Trp Gln Arg Asn Phe Ser Arg Glu Val Glu Gln Leu Leu Arg Lys Gln  
 385 390 395 400

Ser Arg Ile Ala Thr Asn Tyr Asp Ile Tyr Val Phe Ser Ser Ala Ala  
 405 410 415

Leu Asp Asp Ile Leu Ala Lys Phe Ser His Pro Ser Ala Leu Ser Ile  
 420 425 430

Val Ile Gly Val Ala Val Thr Val Leu Tyr Ala Phe Cys Thr Leu Leu  
 435 440 445

Arg Trp Arg Asp Pro Val Arg Gly Gln Ser Ser Val Gly Val Ala Gly  
 450 455 460

Val Leu Leu Met Cys Phe Ser Thr Ala Ala Gly Leu Gly Leu Ser Ala  
 465 470 475 480

Leu Leu Gly Ile Val Phe Asn Ala Leu Thr Ala Ala Tyr Ala Glu Ser  
 485 490 495

Asn Arg Arg Glu Gln Thr Lys Leu Ile Leu Lys Asn Ala Ser Thr Gln  
 500 505 510

Val Val Pro Phe Leu Ala Leu Gly Leu Gly Val Asp His Ile Phe Ile  
 515 520 525

Val Gly Pro Ser Ile Leu Phe Ser Ala Cys Ser Thr Ala Gly Ser Phe  
 530 535 540

Phe Ala Ala Ala Phe Ile Pro Val Pro Ala Leu Lys Val Phe Cys Leu

545	550	555	560
Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val 565		570	575
Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg 580	585		590
Ala Asp Ile Phe Cys Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys 595	600		605
Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Asn Gly Arg Gly Ala 610	615		620
Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Pro Leu Pro Ala Gln 625	630	635	640
Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser 645		650	655
Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro 660		665	670
Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu 675	680		685
Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly 690	695		700
Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe 705	710	715	720
Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val 725		730	735
Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp 740		745	750
Tyr His Asp Ser Phe Val Arg Val Pro His Val Ile Lys Asn Asp Asn 755		760	765
Gly Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly 770	775		780
Asn Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr 785	790	795	800
Lys Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr 805		810	815
Lys Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu 820		825	830
Leu Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln 835		840	845
Arg Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Asp Val Phe 850	855		860

Ala Tyr Gly Ala Ser Gln Gly Lys Leu Tyr Pro Glu Pro Arg Gln Tyr  
 865 870 875 880  
 Phe His Gln Pro Asn Glu Tyr Asp Leu Lys Ile Pro Lys Ser Leu Pro  
 885 890 895  
 Leu Val Tyr Ala Gln Met Pro Phe Tyr Leu His Gly Leu Thr Asp Thr  
 900 905 910  
 Ser Gln Ile Lys Thr Leu Ile Gly His Ile Arg Asp Leu Ser Val Lys  
 915 920 925  
 Tyr Glu Gly Phe Gly Leu Pro Asn Tyr Pro Ser Gly Ile Pro Phe Ile  
 930 935 940  
 Phe Trp Glu Gln Tyr Met Thr Leu Arg Ser Ser Leu Ala Met Ile Leu  
 945 950 955 960  
 Ala Cys Val Leu Leu Ala Ala Leu Val Leu Val Ser Leu Leu Leu Leu  
 965 970 975  
 Ser Val Trp Ala Ala Val Leu Val Ile Leu Ser Val Leu Ala Ser Leu  
 980 985 990  
 Ala Gln Ile Phe Gly Ala Met Thr Leu Leu Gly Ile Lys Leu Ser Ala  
 995 1000 1005  
 Ile Pro Ala Val Ile Leu Ile Leu Ser Val Gly Met Met Leu Cys Phe  
 1010 1015 1020  
 Asn Val Leu Ile Ser Leu Gly Phe Met Thr Ser Val Gly Asn Arg Gln  
 1025 1030 1035 1040  
 Arg Arg Val Gln Leu Ser Met Gln Met Ser Leu Gly Pro Leu Val His  
 1045 1050 1055  
 Gly Met Leu Thr Ser Gly Val Ala Val Phe Met Leu Ser Thr Ser Pro  
 1060 1065 1070  
 Phe Glu Phe Val Ile Arg His Phe Cys Trp Leu Leu Leu Val Val Leu  
 1075 1080 1085  
 Cys Val Gly Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser  
 1090 1095 1100  
 Met Val Gly Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg  
 1105 1110 1115 1120  
 Ile Ser Thr Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly  
 1125 1130 1135  
 Lys Ser Tyr Val Val Gln Gly Ser Arg Ser Ser Arg Gly Ser Cys Gln  
 1140 1145 1150  
 Lys Ser His His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr  
 1155 1160 1165  
 Thr Ile Thr Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile

1170	1175	1180	
Gln Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala			
1185	1190	1195	1200
Ser Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln			
1205	1210	1215	
His His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro			
1220	1225	1230	
Thr Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val			
1235	1240	1245	
Thr Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala			
1250	1255	1260	
Thr Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg			
1265	1270	1275	1280
Ser Tyr Asn Phe Thr Ser			
1285			

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 342 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGTCCATC AGCTTTGGAT ACAGGAAGGT GGTCGCTCG AGCATGAGCT AGCCTACACG	60
CAGAAATCGC TCGCGAGAT GGACTCCTCC ACCGACCAGC TGCTAATCCA AACCCCAAAG	120
ATATGGACGC CTCGATACTG CACCCGAACG CGCTACTGAC GCACCTGGAC GTGGTGAAGA	180
AAGCGATCTC GGTGACGGTG CACATGTACG ACATCACGTG GAGCTCAAGG ACATGTGCTA	240
CTCGCCCAGC ATACCGAGTT CGATACGCAC TTTATCGAGC AGATCTTCGA GAACATCATA	300
CCGTGCGCGA TCATCACGCC GCTGGATTGC TTTTGGGAGG GA	342

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 115 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATGTTAAT ATTCTCATCG

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 1356 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Ala Gly Asn Ala Arg Arg Gly Pro Gly Gln Ala Gly Arg  
 1 5 10 15

Arg Arg Glu Ala Gln Thr Asp Arg Gly Thr Ala Pro Arg Arg Ala Gly  
 20 25 30

Pro Gly Leu Ser Ala Pro Ala Gln Leu Leu Arg Arg Ala Phe Ala Leu  
 35 40 45

Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp  
 50 55 60

Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile  
 65 70 75 80

Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly  
 85 90 95

Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu  
 100 105 110

Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr  
 115 120 125

Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met  
 130 135 140

Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala  
 145 150 155 160

Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val  
 165 170 175

Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser  
 180 185 190

Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr  
 195 200 205

Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly  
 210 215 220

Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu  
 225 230 235 240

Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys  
 245 250 255

Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu  
 260 265 270

Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro  
 275 280 285

Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp  
 290 295 300

Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr

305	310	315	320
Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala			
325		330	335
Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu			
340		345	350
Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val			
355		360	365
Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala			
370		375	380
Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn			
385		390	395
Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Leu Asp Asp Ile			
405		410	415
Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr			
420		425	430
Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys			
435		440	445
Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala			
450		455	460
Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser			
465		470	475
Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val			
485		490	495
Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly			
500		505	510
Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys			
515		520	525
Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala			
530		535	540
Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser			
545		550	555
Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu			
565		570	575
Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg			
580		585	590
Arg Leu Asp Ile Phe Cys Cys Leu Thr Ser Pro Cys Val Ser Arg Val			
595		600	605
Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg			
610		615	620

Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr  
 625 630 635 640  
 His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro  
 645 650 655  
 His Thr His Val Tyr Tyr Thr Ala Glu Pro Arg Ser Glu Ile Ser  
 660 665 670  
 Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro  
 675 680 685  
 Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser  
 690 695 700  
 Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser  
 705 710 715 720  
 Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys  
 725 730 735  
 Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr  
 740 745 750  
 Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro  
 755 760 765  
 Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe  
 770 775 780  
 Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn  
 785 790 795 800  
 Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys  
 805 810 815  
 Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His  
 820 825 830  
 Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp  
 835 840 845  
 Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp  
 850 855 860  
 Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp  
 865 870 875 880  
 Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala  
 885 890 895  
 Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp  
 900 905 910  
 Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg  
 915 920 925  
 Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu

930	935	940
Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe 945 950 955 960		
Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala 965 970 975		
Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu 980 985 990		
Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile 995 1000 1005		
Ser Leu Arg His Trp Leu Leu Ser Ile Ser Val Val Leu Ala Cys 1010 1015 1020		
Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly 1025 1030 1035 1040		
Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met 1045 1050 1055		
Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu 1060 1065 1070		
Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu 1075 1080 1085		
Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala 1090 1095 1100		
Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu 1105 1110 1115 1120		
Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg 1125 1130 1135		
Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn 1140 1145 1150		
Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro 1155 1160 1165		
Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro 1170 1175 1180		
Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr 1185 1190 1195 1200		
Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr 1205 1210 1215		
Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly 1220 1225 1230		
Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro 1235 1240 1245		

Val	Phe	Ala	Arg	Ser	Thr	Val	Val	His	Pro	Asp	Ser	Arg	His	Gln	Pro
1250						1255						1260			
Pro	Leu	Thr	Pro	Arg	Gln	Gln	Pro	His	Leu	Asp	Ser	Gly	Ser	Leu	Ser
1265					1270					1275				1280	
Pro	Gly	Arg	Gln	Gly	Gln	Gln	Pro	Arg	Arg	Asp	Pro	Pro	Arg	Glu	Gly
	1285						1290						1295		
Leu	Arg	Pro	Pro	Pro	Tyr	Arg	Pro	Arg	Arg	Asp	Ala	Phe	Glu	Ile	Ser
		1300					1305						1310		
Thr	Glu	Gly	His	Ser	Gly	Pro	Ser	Asn	Arg	Asp	Arg	Ser	Gly	Pro	Val
			1315				1320					1325			
Gly	Pro	Val	Leu	Thr	Thr	Leu	Gly	Thr	Gln	Arg	Pro	Pro	Pro	Trp	Ala
		1330				1335					1340				
Ala	Leu	Cys	Pro	Ala	Thr	Ala	Ser	Pro	Ser	Pro	Leu				
		1345				1350				1355					

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1356 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Ser	Ala	Gly	Asn	Ala	Arg	Arg	Gly	Pro	Gly	Gln	Ala	Gly	Arg
1				5					10				15		
Arg	Arg	Glu	Ala	Gln	Thr	Asp	Arg	Gly	Thr	Ala	Pro	Arg	Arg	Ala	Gly
				20				25				30			
Pro	Gly	Leu	Ser	Ala	Pro	Ala	Gln	Leu	Leu	Arg	Arg	Ala	Phe	Ala	Leu
				35				40				45			
Glu	Gln	Ile	Ser	Lys	Gly	Lys	Ala	Thr	Gly	Arg	Lys	Ala	Pro	Leu	Trp
				50			55				60				
Leu	Arg	Ala	Lys	Phe	Gln	Arg	Leu	Leu	Phe	Lys	Leu	Gly	Cys	Tyr	Ile
					65		70			75			80		
Gln	Lys	Asn	Cys	Gly	Lys	Phe	Leu	Val	Val	Gly	Leu	Leu	Ile	Phe	Gly
				85				90					95		
Ala	Phe	Ala	Val	Gly	Leu	Lys	Ala	Ala	Asn	Leu	Glu	Thr	Asn	Val	Glu
				100				105					110		
Glu	Leu	Trp	Val	Glu	Val	Gly	Gly	Arg	Val	Ser	Arg	Glu	Leu	Asn	Tyr
				115			120					125			

Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met  
 130 135 140  
 Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala  
 145 150 155 160  
 Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val  
 165 170 175  
 Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser  
 180 185 190  
 Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr  
 195 200 205  
 Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly  
 210 215 220  
 Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu  
 225 230 235 240  
 Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys  
 245 250 255  
 Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu  
 260 265 270  
 Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro  
 275 280 285  
 Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp  
 290 295 300  
 Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr  
 305 310 315 320  
 Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala  
 325 330 335  
 Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu  
 340 345 350  
 Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val  
 355 360 365  
 Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ile Leu Glu Ala  
 370 375 380  
 Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn  
 385 390 395 400  
 Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Leu Asp Asp Ile  
 405 410 415  
 Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr  
 420 425 430  
 Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys

435

440

445

Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala  
 450 455 460  
 Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser  
 465 470 475 480  
 Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val  
 485 490 495  
 Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly  
 500 505 510  
 Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys  
 515 520 525  
 Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala  
 530 535 540  
 Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser  
 545 550 555 560  
 Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu  
 565 570 575  
 Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg  
 580 585 590  
 Arg Leu Asp Ile Phe Cys Cys Leu Thr Ser Pro Cys Val Ser Arg Val  
 595 600 605  
 Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg  
 610 615 620  
 Tyr Ser Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr  
 625 630 635 640  
 His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro  
 645 650 655  
 His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser  
 660 665 670  
 Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro  
 675 680 685  
 Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser  
 690 695 700  
 Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser  
 705 710 715 720  
 Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys  
 725 730 735  
 Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr  
 740 745 750

Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro  
 755 760 765  
 Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe  
 770 775 780  
 Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn  
 785 790 795 800  
 Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys  
 805 810 815  
 Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His  
 820 825 830  
 Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp  
 835 840 845  
 Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp  
 850 855 860  
 Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp  
 865 870 875 880  
 Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala  
 885 890 895  
 Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp  
 900 905 910  
 Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg  
 915 920 925  
 Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu  
 930 935 940  
 Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe  
 945 950 955 960  
 Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala  
 965 970 975  
 Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu  
 980 985 990  
 Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile  
 995 1000 1005  
 Ser Leu Arg His Trp Leu Leu Ser Ile Ser Val Val Leu Ala Cys  
 1010 1015 1020  
 Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly  
 1025 1030 1035 1040  
 Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met  
 1045 1050 1055  
 Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu

1060	1065	1070
Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu		
1075	1080	1085
Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala		
1090	1095	1100
Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu		
1105	1110	1115
Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg		
1125	1130	1135
Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn		
1140	1145	1150
Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro		
1155	1160	1165
Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro		
1170	1175	1180
Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr		
1185	1190	1195
Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr		
1205	1210	1215
Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly		
1220	1225	1230
Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro		
1235	1240	1245
Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro		
1250	1255	1260
Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser		
1265	1270	1275
Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly		
1285	1290	1295
Leu Arg Pro Pro Pro Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser		
1300	1305	1310
Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Val		
1315	1320	1325
Gly Pro Val Leu Thr Thr Leu Gly Thr Gln Arg Pro Pro Pro Trp Ala		
1330	1335	1340
Ala Leu Cys Pro Ala Thr Ala Ser Pro Ser Pro Leu		
1345	1350	1355

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9042 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATCCTGAAT	TGAGAAATAT	AGATTGAAAC	AGAATTCAATT	ACCATTAAAG	CAATCATTAT	60
TTATGGGGGC	GTAATGCGCC	TCCGAGTAGG	CAATGCTTTT	CTTGACATTG	TTACTAAGAA	120
TTGTGAATGA	TATTTGGGCG	TGGATCAACG	CCGATTAAAA	GCTGCTTTG	CTTCCAGGCG	180
GCCAGAGAAG	AGATCCAAAC	TTCAACTCCA	GCCATAAAAG	CAACAACATT	TCCGTCTCCC	240
CCTTGTAGCT	CCCCTTCCTC	CGGCTCTTCC	ACTCTCCACG	AAACGGCAA	TGAAGCTCTC	300
AAAGCGAACT	GTGCTTCGCT	GGTGGTCCAT	TGGCAGCTGC	CGCCACACAG	GCGCTGCTTT	360
TGTGTGTGTG	TGTAATATCA	ATCTTGCTCT	CCCTCTCTTT	TTATCTCTCT	TGGGAATTGG	420
AGCTGCATGC	GAATTGAGCG	ACAGCAAAAC	GAACTGCAAG	TCATTGAGAG	GAGAGCAAAA	480
ACTCGAGCGC	AAGCCAAAGA	TAGCGCAATC	TGGGGAGAGC	GAAATAAAC	TAAAATATGC	540
ATGTTGGAGA	AAAAATGCCG	CCCATGTCGC	CAAAATGCGC	CACACGCAGA	GTGAGCGGGC	600
GGAGGTGGGA	GTAATGGAAA	GGCGATGAG	GGAACGATTA	GCTTGAAGAG	AGAGAACAAAC	660
AAATGAATGT	GCTGCAACGT	TAGTTCAGGT	GAGCGCGTTA	GAGAGAGAGT	TGTTGTTTT	720
TGATTGTAAT	AGCTCGCTTG	GTGGTGGGTC	CACATTACA	TCTCCCTCTC	CCACTCTTTC	780
TCCCCGAAAG	AGAGAGCGGG	ACCGAAGGGG	CACGAGGGG	GCACGATGAC	TATGCAGTTG	840
CATTCAATTT	GAATTTCCAT	GGTGCTGATG	ATTGAGCGC	CAATTTC	GAAGAGTTCT	900
TATTTGTTA	CTTCGTTGTT	GTTGCCTCAA	TTGGAAAGGG	AAAATGTGGA	ATGCGGAGAA	960
ACACCAGAAG	CAAATGCATT	TCCATTCA	AATCCAAAGA	AGTTTAAAG	ATAACATGTC	1020
ATTGGCTTA	AGTCGTTGGT	GCACAAAAAA	GATCGGTTTG	CGGTTGTCGC	ATGAAATGAG	1080
TTTATTCCAT	TGGTATATTA	TTATTCAGAA	ATTAAAAAAA	AACTTGTGTTA	GTCTATTTT	1140
TTTTTTAAA	AAAAAAAAAA	AAATTCTTTT	ATAAGTCGAT	TTTAGAGTAA	ATATTTAAAG	1200
ACTACGTCTA	ATAAACATAT	AATTTGTTCT	GTGTTTAAT	TTGCCGGCAA	AAACAAACCT	1260
ACTTGTGTGG	TCCTCGCACA	CTCATAACCC	CTCGCATATT	TGAGATTCA	GGGGCAAGAG	1320
GCTGCAAAAA	CAATGGAAAG	GGAAAAGCAG	AAACATCCTG	CCGCTCATAA	TTTAGCATCG	1380

GAACATGCAA	AAACAGACAT	CATCGCATGG	GGCAGCAGCA	ACAGCCATAA	AACCAACACG	1440
AGCAATGTAA	AGCTAACAAA	TTTGCACACA	GTTCGCGGCA	CGGCTACACA	CACACACATG	1500
CATGCGCAGC	CTGCCACGCA	CGCGCTTCCC	CCAAACAAAT	ACACACACAC	ACACTGAGAC	1560
GAAAGCTCCA	TTGGGCAGCG	CTGCCGACGC	TGAAGGCCGA	CATCGGCAGA	GCTGAACGTT	1620
TGGGTAGGGG	ACCACCCACA	TCGCTTGCG	GTTTCAGTTT	AATGAAGGCA	GAAACAAATT	1680
TATTTTGGG	TGGTCCACAC	TGCAGCGAAA	ATAAACTACA	GTGGCAACAA	CAAACCAGCA	1740
GCCAAGGCAC	TTTGGGTGGT	CCATGCAAAA	AAAAAAACAAA	TTACGGCATG	CGAATAACAA	1800
TAGAAATTAG	CGCTCTCGTG	GCGGAGCTAT	TTGGGTATAT	TAGAGCTACA	TATTTTATT	1860
GTTTATAAAA	AGTATAAATG	TAAACAATGA	GTTCCAAGCA	TTAAGTCCGT	ATGCTCAACA	1920
ATTACATTAT	CATTATTATT	ATCACTTAAA	TATTTACAAA	GGATATTTAA	ACAGTAATAG	1980
ATATATATTT	TATTTCTTAA	TTTCTGTTAA	CATATGTATT	TACATTGGTA	GTTATTCTTT	2040
ATTTTGCAAC	AAGCATTCA	AAATTTATA	TAACAAACTT	GGTATTTCT	CGGAAAAACT	2100
CCTGAATCAC	CCCTCGGTAT	TTTGTGCGTT	GAGCTATCGT	TAAAGCAGCC	CTCGCAGAGA	2160
GCGTTCTCAA	ACCAAAATGG	CCGCACACGA	AACAAGAGAG	CGAGTGAGAG	TAGGGAGAGC	2220
GTCTGTGTTG	TGTGTTGAGT	GTCGCCACG	CACACAGGCG	CAAACAGTG	CACACAGACG	2280
CCCGCTGGC	AAGAGAGAGT	GAGAGAGAGA	AACAGCGGCG	CGCGCTCGCC	TAATGAAGTT	2340
GTTGGCCTGG	CTGGCGTGCC	GCATCCACGA	GATACAGATA	CATCTCTCAG	ACTGCGTGCG	2400
ATCCTCGAAC	GAAACGGTTG	TAAGTGCAGA	GCGCGACGAC	TTGTTATTG	TATTTCCGAC	2460
TACTGGCACT	CTCTGTGTTG	GGTATACTAA	CAAGATAGAT	ATCACAGAAC	TCGTGGAAAA	2520
GCTAAGATAT	TGTACCTCAC	GGATGCGAGG	CGAAGTTCAT	GGATTAAATG	CCAGGCAACAA	2580
ACAAAAGCCA	GCCAACCAGC	CAGTGTGTTG	GTGTGTGCGT	CGCCAAGTGC	AAAGTAAAGT	2640
AAAGGTAAAA	GAGCGAAAGG	CGAGAGAGAA	AACCGAATAC	GTGAGTCGTC	CGACTGCCGC	2700
TTTCCATGT	GTAAAAGATC	TGTGAAATT	CTGTCAAATT	CCCCTGAGAA	ATTGTGCCCA	2760
AGATAAAACC	CGAAAACCGC	GTGTTAACG	TCGAAAAAAC	CCAGCAAAAG	CGAAGCCAGC	2820
AATCACAAACA	AAACAACATA	ACGAGAGCTC	AGATACACAG	CGTGCTCAGT	GAGTGAGCGA	2880
GAGAGCGCGG	GAGAGAGCGT	CTCTTGATT	AAAATACAAA	ATAATTAAAA	ATAAAAATGC	2940
GGAATGCAGT	GCAAAATGCA	GCCAAACAAA	ATACGAGATT	CCAATAACAA	TTAATCGAAC	3000
CGAAAGTCCA	CGAACAAATCC	GCACACTGTC	TCCCAAGTCT	CAGTTCTCAG	GACGCAGACG	3060
AACGGCAGGC	ACTGTAGAAA	GACCGATTCC	GCAGCACACT	CCCATCTGCA	CATCTCCGCC	3120

ACCGCGATTCC	GTCCGGAATC	TGGCTATAAA	CATAACCATA	ATGGACCGCG	ACAGCCTCCC	3180
ACCGCGTTCCG	GACACACACG	GCGATGTGGT	CGATGAGAAA	TTATTCTCGG	ATCTTACAT	3240
ACGCACCAGC	TGGGTGGACG	CCCAAGTGGC	GCTCGATCAG	ATAGATAAGG	TGAGTGCCA	3300
ACTACAGTGA	ACTTTCACTG	TGAAGGATAG	CCATGTGTTG	AATTCAATAA	TATTCTTGAT	3360
CGTATTCCGA	GGATCCAATT	TTAATGCGTA	TTTTATGGCA	GTGGAGCAAG	GCGGGGGAAT	3420
CTAAAAAAA	AACTAACGC	TAAATTCCGT	ATTTTGTTG	CATTTTCAG	GGCAAAGCGC	3480
GTGGCAGCCG	CACGGCGATC	TATCTGCGAT	CAGTATTCCA	GTCCCACCTC	GAAACCCTCG	3540
GCAGCTCCGT	GCAAAAGCAC	GCGGGCAAGG	TGCTATTCGT	GGCTATCCTG	GTGCTGAGCA	3600
CCTTCTGCGT	CGGCCTGAAG	AGCGCCCAGA	TCCACTCCAA	GGTGCACCAG	CTGTGGATCC	3660
AGGAGGGCGG	CCGGCTGGAG	GCGGAACTGG	CCTACACACA	GAAGACGATC	GGCGAGGACG	3720
AGTCGGCCAC	GCATCAGCTG	CTCATTCTAGA	CGACCCACGA	CCCGAACGCC	TCCGTCTGC	3780
ATCCGCAGGC	GCTGCTTGCC	CACCTGGAGG	TCCTGGTCAA	GGCCACCGCC	GTCAAGGTGC	3840
ACCTCTACGA	CACCGAATGG	GGGCTGCGCG	ACATGTCAA	CATGCCGAGC	ACGCCCTCCT	3900
TCGAGGGCAT	CTACTACATC	GAGCAGATCC	TGCGCCACCT	CATTCCGTGC	TCGATCATCA	3960
CGCCGCTGGA	CTGTTCTGG	GAGGGAAGCC	AGCTGTTGGG	TCCGGAATCA	GCGGTCGTTA	4020
TACCGTAAGT	AGTTAATATG	TAGTTAATAG	CCACATCTTA	TAGATTCTAA	AGTGAACGTA	4080
TCCCTTATGA	CCATATCCTT	TTGCATGATC	TACTTTAAC	CACAGTACTT	CTCTATTCAT	4140
ATTAAGGAAT	TAATAAAGTA	CTTACTTTGC	GCTTACCTTT	ATTAATACG	ATAGCTTATC	4200
TTTATAAACT	TGCTATCAAG	TCGAAAGATA	AACGTGACAA	GAGTATCTT	GTACTTATCC	4260
CAGTTGCTTA	CCATCGTAAA	TAATCTTCTT	ATTAATAAT	ATTCGTAAAT	AAATATTCTT	4320
AACTCAACAA	ATCCATCTT	ATTATTGTTA	CTCCTCTACA	GAGGCCTCAA	CCAACGACTC	4380
CTGTGGACCA	CCCTGAATCC	CGCCTCTGTG	ATGCAGTATA	TGAAACAAAA	GATGTCCGAG	4440
GAAAAGATCA	GCTTCGACTT	CGAGACCGTG	GAGCAGTACA	TGAAGCGTGC	GGCCATTGGC	4500
AGTGGCTACA	TGGAGAAGCC	CTGCCTGAAC	CCACTGAATC	CCAATTGCC	GGACACGGCA	4560
CCGAACAAAGA	ACAGCACCCA	GCCGCCGGAT	GTGGGAGCCA	TCCTGTCCGG	AGGCTGCTAC	4620
GGTTATGCCG	CGAAGCACAT	GCACTGGCCG	GAGGAGCTGA	TTGTGGGCGG	ACGGAAGAGG	4680
AACCGCAGCG	GACACTTGAG	GAAGGCCAG	GCCCTGCAGT	CGGTGGTGCA	GCTGATGACC	4740
GAGAAGGAAA	TGTACGACCA	GTGGCAGGAC	AACTACAAGG	TGCACCATCT	TGGATGGACG	4800
CAGGAGAAGG	CAGCGGAGGT	TTTGAACGCC	TGGCAGCGA	ACTTTCGCG	GGAGGTGGAA	4860

CAGCTGCTAC	GTAAACAGTC	GAGAATTGCC	ACCAACTACG	ATATCTACGT	GTTCAGCTCG	4920
GCTGCACTGG	ATGACATCCT	GGCCAAGTTC	TCCCATCCCA	GCGCCTTGTG	CATTGTCATC	4980
GGCGTGGCCG	TCACCGTTT	GTATGCCTT	TGCACGCTCC	TCCGCTGGAG	GGACCCCGTC	5040
CGTGGCCAGA	GCAGTGTGGG	CGTGGCCGG	GTTCTGCTCA	TGTGCTTCAG	TACCGCCGCC	5100
GGATTGGGAT	TGTCAGCCCT	GCTCGGTATC	GTTCATCAATG	CGCTGACCAC	TGCCTATGCG	5160
GAGAGCAATC	GGCGGGAGCA	GACCAAGCTG	ATTCTCAAGA	ACGCCAGCAC	CCAGGTGGTT	5220
CCGTTTTGG	CCCTTGGTCT	GGGCGTCGAT	CACATCTTCA	TAGTGGGACC	GAGCATCCTG	5280
TTCAGTGCCT	GCAGCACCAC	AGGATCCTTC	TTTGCGGCCG	CCTTTATTCC	GGTGCCGGCT	5340
TTGAAGGTAT	TCTGTCTGCA	GGCTGCCATC	GTAATGTGCT	CCAATTGTC	AGCGGCTCTA	5400
TTGGTTTTTC	CGGCCATGAT	TTCGTTGGAT	CTACGGAGAC	GTACCGCCGG	CAGGGCGGAC	5460
ATCTTCTGCT	GCTGTTTCC	GGTGTGGAAG	GAACAGCCGA	AGGTGGCACC	TCCGGTGCTG	5520
CCGCTGAACA	ACAACAACGG	GCGCGGGGCC	CGGCATCCGA	AGAGCTGCAA	CAACAACAGG	5580
GTGCCGCTGC	CCGCCCAGAA	TCCTCTGCTG	GAACAGAGGG	CAGACATCCC	TGGGAGCAGT	5640
CACTCACTGG	CGTCCTTCTC	CCTGGCAACC	TTCGCCTTTC	AGCACTACAC	TCCCTTCCCTC	5700
ATGCGCAGCT	GGGTGAAGTT	CCTGACCGTT	ATGGGTTTCC	TGGCGGCCCT	CATATCCAGC	5760
TTGTATGCCT	CCACGCGCCT	TCAGGATGGC	CTGGACATTA	TTGATCTGGT	GCCCAAGGAC	5820
AGCAACGAGC	ACAAGTTCCCT	GGATGCTCAA	ACTCGGCTCT	TTGGCTTCTA	CAGCATGTAT	5880
GCGGTTACCC	AGGGCAACTT	TGAATATCCC	ACCCAGCAGC	AGTTGCTCAG	GGACTACCAC	5940
GATTCTTTG	TGCGGGTGCC	ACATGTGATC	AAGAATGATA	ACGGTGGACT	GCCGGACTTC	6000
TGGCTGCTGC	TCTTCAGCGA	GTGGCTGGGT	AATCTGAAA	AAGATATTG	ACGAGGAATA	6060
CCGCGACGGA	CGGCTGGACC	AAGGAGTGCT	GGTTCCAAA	CGCCAGCAGC	GATGCCATC	6120
CTGGCCTACA	AGCTAACCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGG	CAAGGAAC	6180
GTGCTCACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCC	CTTCTACAAC	6240
TATCTGTCGG	CATGGGCCAC	CAACGACGTC	TTCGCCTACG	GAGCTTCTCA	GGTGGGTCTT	6300
CTTATTAAAT	TAAATTAAAT	TAAATTAAAT	TAGATGCCCT	TAGTTCTCCT	CATATGTACA	6360
TACATATTAT	AACTTATCGC	ACTCCAAAGT	TAAAGATTAC	TAAATGTGTG	TGTATCTTA	6420
TTCTTACAGG	GCAAATTGTA	TCCGGAACCG	CGCCAGTATT	TTCACCAACC	CAACGAGTAC	6480
GATCTTAAGA	TACCCAAGAG	TCTGCCATTG	GTCTACGCTC	AGATGCCCTT	TTACCTCCAC	6540
GGACTAACAG	ATACCTCGCA	GATCAAGACC	CTGATAGGTC	ATATTGCGA	CCTGAGCGTC	6600

AAGTACGAGG GCTTCGGCCT GCCCAACTAT CCATCGGGTG AGTCGGAAAT GAGTACTTCA	6660
TACATGGGGC CCAACTAAC A GTCGATTAT TTATGCCAG GCATTCCCTT CATCTTCTGG	6720
GAGCAGTACA TGACCCTGCG CTCCTCACTG GCCATGATCC TGGCCTGCCT GCTACTCGCC	6780
GCCCTGGTGC TGGTCTCCCT GCTCCTGCTC TCCGTTGGG CCGCCGTTCT CGTGATCCTC	6840
AGCGTTCTGG CCTCGCTGGC CCAGATCTT GGGGCCATGA CTCTGCTGGG CATCAAACTC	6900
TCGGCCATTC CGGCAGTCAT ACTCATCCTC AGCGTGGCA TGATGCTGTG CTTCAATGTG	6960
CTGATATCAC TGGTGAGTCT TCATTTCTGG CTGGACCATT AAGAGCTTCG GAGTGAGTCT	7020
TCATTTCTGG CTGGACCATT AAGAGCTTCG GAGTGAGTCT TCATTTCTGG CTGGACCATT	7080
AAGAGCTTCG GATTTCCAG AGATATCCA AGACTTTCA TTGGATCCTC TTCAGCACAC	7140
ATTAATTGCT TATCTTCCG ATTCTAGGGC TTCATGACAT CCGTTGGCAA CCGACAGCGC	7200
CGCGTCCAGC TGAGCATGCA GATGTCCCTG GGACCACTTG TCCACGGCAT GCTGACCTCC	7260
GGAGTGGCCG TGTTCATGCT CTCCACGTG TG CCCTTGAGT TTGTGATCCG GCACTTCTGC	7320
TGGCTTCTGC TGGTGGTCTT ATGCGTTGGC GCCTGCAACA GCCTTTGGT GTTCCCCATC	7380
CTACTGAGCA TGGTGGGACC GGAGGCGGAG CTGGTGCCGC TGGAGCATCC AGACCGCATA	7440
TCCACGCCCT CTCCGCTGCC CGTGCAGC AGCAAGAGAT CGGGCAAATC CTATGTGGTG	7500
CAGGGATCGC GATCCTCGCG AGGCAGCTGC CAGAAGTCGC ATCACCACCA CCACAAAGAC	7560
CTTAATGATC CATCGCTGAC GACGATCACC GAGGAGCCGC AGTCGTGGAA GTCCAGCAAC	7620
TCGTCCATCC AGATGCCAA TGATTGGACC TACCAGCCGC GGGAACAGCG ACCCGCCTCC	7680
TACGCGGGCCC CGCCCCCGC CTATCACAAG GCCGCCGCC AGCAGCACCA CCAGCATCAG	7740
GGCCCGCCCA CAACGCCCA GCCTCCCTTC CCGACGGCCT ATCCGCCGGA GCTGCAGAGC	7800
ATCGTGGTGC AGCCGGAGGT GACGGTGGAG ACGACGCACT CGGACAGCAA CACCACCAAG	7860
GTGACGGCCA CGGCCAACAT CAAGGTGGAG CTGGCCATCC CGGCAGGCAG TGCGCAGCTA	7920
TAACTTACG AGTTAGCACT AGCACTAGTT CCTGTAGCTA TTAGGACGTA TCTTTAGACT	7980
CTAGCCTAACAG CCGTAACCCCT ATTTGTATCT GTAAAATCGA TTTGTCCAGC GGGTCTGCTG	8040
AGGATTCGT TCTCATGGAT TCTCATGGAT TCTCATGGAT GCTTAAATGG CATGGTAATT	8100
GGCAAAATAT CAATTTTGT GTCTAAAAA GATGCATTAG CTTATGGTTT CAAGATAACAT	8160
TTTAAAGAG TCCGCCAGAT ATTTATATAA AAAAATCCA AAATCGACGT ATCCATGAAA	8220
ATTGAAAAGC TAAGCAGACC CGTATGTATG TATATGTGTA TGCATGTTAG TTAATTCCC	8280
GAAGTCCGGT ATTTATAGCA GCTGCCTTCC GCGCCCCCT TCCCTTGAAA TGAACACCCT	8340

TCCAGCCACG	CCCCACCGCC	CCTCTGCGTA	GCAGCTTGT	ATGTATGTAG	TATGCTAGCA	8400		
CCTAAGGAAT	ACTTAAACTT	AGAGATATT	ATTGTAACAC	ACGAAAACA	CACACAATGT	8460		
ACTTACATAT	AATTCAATGC	GAGATTCA	CACACAAAAA	GGAAACACAA	CAAAC	8520		
ATTGTAGCTC	GTAATTAGT	TTAAATATGT	TACATAAAAC	ACAAGGACTT	GAACCAAAAT	8580		
AGTATCGCTT	AAACGGAAAC	GAGAGAAACG	AGAAAAAATA	ACTATTACTT	AATCAACTAC	8640		
AAGAGAGATA	TCCCTCCTCC	CCTAACCGTA	CTTACAACCA	AAATAAAACA	AGAGTATAAG	8700		
CATAAAAATG	GAAAACGAAG	CGAGGAACGA	TTGTAAACGC	GGTCATTTAT	CCTGTACATT	8760		
TGTTGCCCGA	AGACTGACTG	TCTTTTTTT	AATAAAAATA	TATATTATAC	AGTTTTTAA	8820		
AAGCGAAATT	CATGACTTTT	TTTAACAGT	GAGCAGAGAA	CAAAGAAC	GGAAGTTTC	8880		
GCTGTATCAA	TAAAAAGATT	CCATTTTTT	AATAAATTGT	AAAATCCTA	AAAAAAAGAA	8940		
GA	CTACAAAAA	GT	TTAAATT	TTATACGTTA	TTGATAAACT	TTTATACACG	AAAATACTG	9000
TA	CTT	AGCTA	TGATCAACTC	CTGGCTTAA	GTCTGGGTA	AG	9042	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile	Ile	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly
1				5					10	

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu	Ile	Val	Gly	Gly
1			5	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Pro Phe Phe Trp Glu Gln Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGACGAATTC AAGTCACATT GG

22

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGACGAATTC CTCCCAAACA TC

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGACGAATTC TGATGTTGG GA

22

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGACGAATTC TGATGTTGG GA

22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATACCAGCC AAGCTTGTCT GCCATGCAT

29